

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/623,808
Source: IFW
Date Processed by STIC: 02/08/2006

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/623,808DATE: 02/08/2006
TIME: 13:06:17

INPUT SET: S30752.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>
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SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Alderson, Mark R.
Goodwin, Raymond G.
Smith, Craig A.

(ii) TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: US
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Power Macintosh
(C) OPERATING SYSTEM: Apple 7.5.3
(D) SOFTWARE: Microsoft Word, Version #6.0.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/623,808
(B) FILING DATE: 22-JUL-2003
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/236,918
(B) FILING DATE: 06-May-1994
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/060,843
(B) FILING DATE: 07-May-1993
(C) CLASSIFICATION: 435

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Anderson, Kathryn A.
(B) REGISTRATION NUMBER: 32,172
(C) REFERENCE/DOCKET NUMBER: 2801-B

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47
48 (ix) TELECOMMUNICATION INFORMATION:
49 (A) TELEPHONE: (206) 587-0430
50 (B) TELEFAX: (206) 233-0644
51
52
53 (2) INFORMATION FOR SEQ ID NO:1:
54
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 1254 base pairs
57 (B) TYPE: nucleic acid
58 (C) STRANDEDNESS: single
59 (D) TOPOLOGY: linear
60
61 (ii) MOLECULE TYPE: cDNA to mRNA
62
63 (iii) HYPOTHETICAL: NO
64
65 (iv) ANTI-SENSE: NO
66
67
68 (vii) IMMEDIATE SOURCE:
69 (B) CLONE: murine 4-1BB-L
70
71 (ix) FEATURE:
72 (A) NAME/KEY: CDS
73 (B) LOCATION: 53..979
74
75
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
77
78 AGCCTATAAA GCACGGGCAC TGGCGGGAGA CGTGCACTGA CCGACCGTGG TA ATG 55
79 Met
80 1
81
82 GAC CAG CAC ACA CTT GAT GTG GAG GAT ACC GCG GAT GCC AGA CAT CCA 103
83 Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His Pro
84 5 10 15
85
86 GCA GGT ACT TCG TGC CCC TCG GAT GCG GCG CTC CTC AGA GAT ACC GGG 151
87 Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly
88 20 25 30
89
90 CTC CTC GCG GAC GCT GCG CTC CTC TCA GAT ACT GTG CGC CCC ACA AAT 199
91 Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn
92 35 40 45
93
94 GCC GCG CTC CCC ACG GAT GCT GCC TAC CCT GCG GTT AAT GTT CGG GAT 247
95 Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp
96 50 55 60 65
97
98 CGC GAG GCC GCG TGG CCG CCT GCA CTG AAC TTC TGT TCC CGC CAC CCA 295
99 Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro

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	70	75	80	
100				
101				
102	AAG CTC TAT GGC CTA GTC GCT TTG GTT TTG CTG CTT CTG ATC GCC GCC			343
103	Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala Ala			
104	85	90	95	
105				
106	TGT GTT CCT ATC TTC ACC CGC ACC GAG CCT CGG CCA GCG CTC ACA ATC			391
107	Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile			
108	100	105	110	
109				
110	ACC ACC TCG CCC AAC CTG GGT ACC CGA GAG AAT AAT GCA GAC CAG GTC			439
111	Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val			
112	115	120	125	
113				
114	ACC CCT GTT TCC CAC ATT GGC TGC CCC AAC ACT ACA CAA CAG GGC TCT			487
115	Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser			
116	130	135	140	145
117				
118	CCT GTG TTC GCC AAG CTA CTG GCT AAA AAC CAA GCA TCG TTG TGC AAT			535
119	Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn			
120	150	155	160	
121				
122	ACA ACT CTG AAC TGG CAC AGC CAA GAT GGA GCT GGG AGC TCA TAC CTA			583
123	Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu			
124	165	170	175	
125				
126	TCT CAA GGT CTG AGG TAC GAA GAA GAC AAA AAG GAG TTG GTG GTA GAC			631
127	Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp			
128	180	185	190	
129				
130	AGT CCC GGG CTC TAC TAC GTA TTT TTG GAA CTG AAG CTC AGT CCA ACA			679
131	Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr			
132	195	200	205	
133				
134	TTC ACA AAC ACA GGC CAC AAG GTG CAG GGC TGG GTC TCT CTT GTT TTG			727
135	Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu			
136	210	215	220	225
137				
138	CAA GCA AAG CCT CAG GTA GAT GAC TTT GAC AAC TTG GCC CTG ACA GTG			775
139	Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val			
140	230	235	240	
141				
142	GAA CTG TTC CCT TGC TCC ATG GAG AAC AAG TTA GTG GAC CGT TCC TGG			823
143	Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp			
144	245	250	255	
145				
146	AGT CAA CTG TTG CTC CTG AAG GCT GGC CAC CGC CTC AGT GTG GGT CTG			871
147	Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu			
148	260	265	270	
149				
150	AGG GCT TAT CTG CAT GGA GCC CAG GAT GCA TAC AGA GAC TGG GAG CTG			919
151	Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu			
152	275	280	285	

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153
154 TCT TAT CCC AAC ACC ACC AGC TTT GGA CTC TTT CTT GTG AAA CCC GAC      967
155 Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp
156 290                      295                      300                      305
157
158 AAC CCA TGG GAA TGAGAACTAT CCTTCTTGTG ACTCCTAGTT GCTAAGTCCT      1019
159 Asn Pro Trp Glu
160
161
162 CAAGCTGCTA TGTTTTATGG GGTCTGAGCA GGGGTCCCTT CCATGACTTT CTCTTGTCTT      1079
163
164 TAACTGGACT TGGTATTTAT TCTGAGCATA GCTCAGACAA GACTTTATAT AATTCAC TAG      1139
165
166 ATAGCATTAG TAAACTGCTG GGCAGCTGCT AGATAAAAAA AAATTCTAA ATCAAAGTTT      1199
167
168 ATATTTATAT TAATATATAA AAATAAATGT GTTTGTAAAT AAAAAAAAAA AAAAA      1254
169
170
171 (2) INFORMATION FOR SEQ ID NO:2:
172
173     (i) SEQUENCE CHARACTERISTICS:
174         (A) LENGTH: 309 amino acids
175         (B) TYPE: amino acid
176         (D) TOPOLOGY: linear
177
178     (ii) MOLECULE TYPE: protein
179
180     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
181
182 Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
183   1           5           10           15
184
185 Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
186           20           25           30
187
188 Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
189           35           40           45
190
191 Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
192           50           55           60
193
194 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
195           65           70           75           80
196
197 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala
198           85           90           95
199
200 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
201           100          105          110
202
203 Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
204           115          120          125
205

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206 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
207      130                      135                      140
208
209 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
210      145                      150                      155                      160
211
212 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
213                      165                      170                      175
214
215 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
216                      180                      185                      190
217
218 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
219                      195                      200                      205
220
221 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
222      210                      215                      220
223
224 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
225      225                      230                      235                      240
226
227 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
228                      245                      250                      255
229
230 Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
231                      260                      265                      270
232
233 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
234                      275                      280                      285
235
236 Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
237      290                      295                      300
238
239 Asp Asn Pro Trp Glu
240      305

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: human 4-1BB-L(7A)

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/10/623,808DATE: 02/08/2006
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Line	Error	Original Text
30	Wrong Classification	(C) CLASSIFICATION:435
35	Wrong Classification	(C) CLASSIFICATION:435
40	Wrong Classification	(C) CLASSIFICATION:435

PAGE: 1

SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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Line	Original Text	Corrected Text
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/10/623,808DATE: 02/08/2006
TIME: 13:06:18***INPUT SET: S30752.raw***

Line	Error	Original Text
30	Wrong Classification	(C) CLASSIFICATION:435
35	Wrong Classification	(C) CLASSIFICATION:435
40	Wrong Classification	(C) CLASSIFICATION:435

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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/10/623,808

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<< THERE ARE NO ITEMS MISSING >>

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SEQUENCE CORRECTION REPORT
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Line	Original Text	Corrected Text
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